SEQUENCE LISTING

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Epicyte Pharmaceutical, Inc.

<120> Plant production of immunoglobulins with reduced fucosylation

<130> 38136-5001-WO

<150> US 60/429,385
<151> 2002-11-27

<160> 85

<170> PatentIn version 3.1

<210> 1
<211> 1494
<212> DNA
<213> Herpes simplex virus

<220>
<221> CDS
<222> (1)..(1494)
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<221> misc_feature
<223> HSV Heavy Chain sequence

<400> 1

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Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly
1               5                   10                  15

gtc cat tgc cag gtt cag ctc gtg cag tca ggt gct gag gtg aag aag        96
Val His Cys Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
                20                  25                  30

cct ggc tcc tcg gtg aag gtc tcc tgc aag gct tct gga ggt tcc ttc       144
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Ser Phe
            35                  40                  45

agc tcc tat gct atc aac tgg gtg agg caa gct cct gga caa ggg ctt       192
Ser Ser Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
        50                  55                  60

gag tgg atg gga ggg ctc atg cct atc ttt ggg aca aca aac tac gcg       240
Glu Trp Met Gly Gly Leu Met Pro Ile Phe Gly Thr Thr Asn Tyr Ala
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        65                    70                    75                    80

cag aag ttc cag gac agg ctc acg att acc gcg gac gta tcc acg agt     288
Gln Lys Phe Gln Asp Arg Leu Thr Ile Thr Ala Asp Val Ser Thr Ser
                    85                    90                    95

aca gcc tac atg caa ctg agc ggc ctg aca tat gaa gac acg gcc atg     336
Thr Ala Tyr Met Gln Leu Ser Gly Leu Thr Tyr Glu Asp Thr Ala Met
                100                   105                   110

tat tac tgt gcg aga gtt gcc tac atg ctt gaa cct acc gtc act gca     384
Tyr Tyr Cys Ala Arg Val Ala Tyr Met Leu Glu Pro Thr Val Thr Ala
                115                   120                   125

ggt ggt ttg gac gtc tgg ggc caa ggg acc ttg gtc acc gtc tcc tcc     432
Gly Gly Leu Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        130                   135                   140

gca tcc ccg acc agc ccg aag gtc ttc ccg ctg agc ctc tgt agc acc     480
Ala Ser Pro Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Cys Ser Thr
145                   150                   155                   160

cag cca gat ggg aac gtg gtc atc gcc tgc ctg gtc cag ggc ttc ttc     528
Gln Pro Asp Gly Asn Val Val Ile Ala Cys Leu Val Gln Gly Phe Phe
                    165                   170                   175

cct cag gag cca ctc agt gtg acc tgg agc gaa agc gga cag ggc gtg     576
Pro Gln Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Gly Val
                180                   185                   190

acc gcc agg aac ttc cca ccc agc cag gat gcc tcc gga gac ctg tac     624
Thr Ala Arg Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr
                195                   200                   205

acc acg tcc agc cag ctg acc ctt ccg gcc aca cag tgc cta gcg ggc     672
Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Leu Ala Gly
        210                   215                   220

aag tcc gtg aca tgc cac gtg aag cac tac acg aat ccc agc cag gat     720
Lys Ser Val Thr Cys His Val Lys His Tyr Thr Asn Pro Ser Gln Asp
225                   230                   235                   240

gtg act gtg ccc tgc cca gtt ccc tca act cca cct acc cca tct ccc     768
Val Thr Val Pro Cys Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro
                    245                   250                   255

tcg act cca cct acc cca tct ccc tca tgc tgc cac ccc agg ctg tca     816
Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser
                260                   265                   270

ctg cac agg cct gcc ctc gag gac ctg ctc tta ggt tcg gaa gcg aac     864
Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Asn
                275                   280                   285

ctc acg tgc aca ctc acc ggc ctg aga gat gcg tca ggt gtc acc ttc     912
Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe
        290                   295                   300

acc tgg acg ccc tca agt ggt aag agc gct gtt caa ggc cca cct gag     960
Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Glu
305                   310                   315                   320
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cgt gac ctc tgt ggc tgc tac agc gtg tcc agt gtc ctt ccg ggc tgt    1008
Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys
                325              330              335

gcc gag cct tgg aat cat ggg aag acc ttc act tgc act gct gcc tac    1056
Ala Glu Pro Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr
                340              345              350

ccc gag agc aag acc ccg cta acc gcc acc ctc tcg aaa tcc ggc aac    1104
Pro Glu Ser Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn
                355              360              365

aca ttc cgg ccc gag gtc cac ctg ctg ccg ccg ccg tcg gag gag ctg    1152
Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu
        370              375              380

gcc ctg aac gag ctg gtg acg ctg acg tgc ctg gcg cgc ggc ttc agc    1200
Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser
385              390              395              400

ccc aag gac gtg ctg gtt cgc tgg ctg cag ggc tca cag gag ctg cct    1248
Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro
                405              410              415

agg gag aag tac ctg act tgg gca tcc cgg cag gag ccc agc caa ggc    1296
Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly
                420              425              430

acc acc acc ttc gct gtg acc tcg ata ctg cgc gtg gca gcc gag gac    1344
Thr Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp
                435              440              445

tgg aag aag ggt gac acc ttc tcc tgc atg gtg ggc cac gag gcc ctt    1392
Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu
        450              455              460

ccg ctg gcc ttc aca cag aag acc atc gac cgc ttg gcg ggt aaa ccc    1440
Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro
465              470              475              480

acc cat gtc aat gtg tct gtt gtc atg gcg gag gtg gac ggc acc tgc    1488
Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp Gly Thr Cys
                485              490              495

tac tga                                                            1494
Tyr
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<210>   2
<211>   497
<212>   PRT
<213>   Herpes simplex virus

<400>   2
Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly
1               5               10              15

Val His Cys Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20              25              30
```

```
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Ser Phe
        35              40              45

Ser Ser Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
        50              55              60

Glu Trp Met Gly Gly Leu Met Pro Ile Phe Gly Thr Thr Asn Tyr Ala
65              70              75              80

Gln Lys Phe Gln Asp Arg Leu Thr Ile Thr Ala Asp Val Ser Thr Ser
                85              90              95

Thr Ala Tyr Met Gln Leu Ser Gly Leu Thr Tyr Glu Asp Thr Ala Met
            100             105             110

Tyr Tyr Cys Ala Arg Val Ala Tyr Met Leu Glu Pro Thr Val Thr Ala
        115             120             125

Gly Gly Leu Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
    130             135             140

Ala Ser Pro Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Cys Ser Thr
145             150             155             160

Gln Pro Asp Gly Asn Val Val Ile Ala Cys Leu Val Gln Gly Phe Phe
                165             170             175

Pro Gln Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Gly Val
        180             185             190

Thr Ala Arg Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr
        195             200             205

Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Leu Ala Gly
    210             215             220

Lys Ser Val Thr Cys His Val Lys His Tyr Thr Asn Pro Ser Gln Asp
225             230             235             240

Val Thr Val Pro Cys Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro
            245             250             255

Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser
        260             265             270

Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Asn
        275             280             285

Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe
    290             295             300

Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Glu
305             310             315             320

Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys
            325             330             335

Ala Glu Pro Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr
        340             345             350

Pro Glu Ser Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn
```

```
                355                    360                    365
      Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu
          370              375              380
      Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser
      385              390              395              400
      Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro
              405              410              415
      Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly
              420              425              430
      Thr Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp
          435              440              445
      Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu
          450              455              460
      Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro
      465              470              475              480
      Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp Gly Thr Cys
                  485              490              495
      Tyr
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<210> 3
<211> 57
<212> DNA
<213> Artificial sequence

<220>
<223> Heavy chain signal peptide

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<221> CDS
<222> (1)..(57)
<223>

<400> 3
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Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly
1               5                   10                  15

gtc cat tgc                                                            57
Val His Cys
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<210> 4
<211> 19
<212> PRT
<213> Artificial sequence

<220>
<223> Heavy chain signal peptide

<400> 4

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Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly
1               5                   10                  15

Val His Cys
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<210> 5
<211> 1368
<212> DNA
<213> Artificial sequence

<220>
<223> Mature heavy chain sequence

<220>
<221> CDS
<222> (1)..(1368)
<223>

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<400> 5
cag gtt cag ctc gtg cag tca ggt gct gag gtg aag aag cct ggc tcc      48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15

tcg gtg aag gtc tcc tgc aag gct tct gga ggt tcc ttc agc tcc tat      96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Ser Phe Ser Ser Tyr
            20                  25                  30

gct atc aac tgg gtg agg caa gct cct gga caa ggg ctt gag tgg atg     144
Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

gga ggg ctc atg cct atc ttt ggg aca aca aac tac gcg cag aag ttc     192
Gly Gly Leu Met Pro Ile Phe Gly Thr Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60

cag gac agg ctc acg att acc gcg gac gta tcc acg agt aca gcc tac     240
Gln Asp Arg Leu Thr Ile Thr Ala Asp Val Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

atg caa ctg agc ggc ctg aca tat gaa gac acg gcc atg tat tac tgt     288
Met Gln Leu Ser Gly Leu Thr Tyr Glu Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

gcg aga gtt gcc tac atg ctt gaa cct acc gtc act gca ggt ggt ttg     336
Ala Arg Val Ala Tyr Met Leu Glu Pro Thr Val Thr Ala Gly Gly Leu
            100                 105                 110

gac gtc tgg ggc caa ggg acc ttg gtc acc gtc tcc tcc gca tcc ccg     384
Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Pro
        115                 120                 125

acc agc ccg aag gtc ttc ccg ctg agc ctc tgt agc acc cag cca gat     432
Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Cys Ser Thr Gln Pro Asp
    130                 135                 140

ggg aac gtg gtc atc gcc tgc ctg gtc cag ggc ttc ttc cct cag gag     480
Gly Asn Val Val Ile Ala Cys Leu Val Gln Gly Phe Phe Pro Gln Glu
145                 150                 155                 160

cca ctc agt gtg acc tgg agc gaa agc gga cag ggc gtg acc gcc agg     528
```

```
      Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Gly Val Thr Ala Arg
                      165             170             175

      aac ttc cca ccc agc cag gat gcc tcc gga gac ctg tac acc acg tcc        576
      Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr Thr Thr Ser
                  180             185             190

      agc cag ctg acc ctt ccg gcc aca cag tgc cta gcg ggc aag tcc gtg        624
      Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Leu Ala Gly Lys Ser Val
                  195             200             205

      aca tgc cac gtg aag cac tac acg aat ccc agc cag gat gtg act gtg        672
      Thr Cys His Val Lys His Tyr Thr Asn Pro Ser Gln Asp Val Thr Val
          210             215             220

      ccc tgc cca gtt ccc tca act cca cct acc cca tct ccc tcg act cca        720
      Pro Cys Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro
      225             230             235             240

      cct acc cca tct ccc tca tgc tgc cac ccc agg ctg tca ctg cac agg        768
      Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser Leu His Arg
                      245             250             255

      cct gcc ctc gag gac ctg ctc tta ggt tcg gaa gcg aac ctc acg tgc        816
      Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Asn Leu Thr Cys
                  260             265             270

      aca ctc acc ggc ctg aga gat gcg tca ggt gtc acc ttc acc tgg acg        864
      Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe Thr Trp Thr
                  275             280             285

      ccc tca agt ggt aag agc gct gtt caa ggc cca cct gag cgt gac ctc        912
      Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Glu Arg Asp Leu
          290             295             300

      tgt ggc tgc tac agc gtg tcc agt gtc ctt ccg ggc tgt gcc gag cct        960
      Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala Glu Pro
      305             310             315             320

      tgg aat cat ggg aag acc ttc act tgc act gct gcc tac ccc gag agc       1008
      Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser
                      325             330             335

      aag acc ccg cta acc gcc acc ctc tcg aaa tcc ggc aac aca ttc cgg       1056
      Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg
                  340             345             350

      ccc gag gtc cac ctg ctg ccg ccg ccg tcg gag gag ctg gcc ctg aac       1104
      Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn
                  355             360             365

      gag ctg gtg acg ctg acg tgc ctg gcg cgc ggc ttc agc ccc aag gac       1152
      Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp
          370             375             380

      gtg ctg gtt cgc tgg ctg cag ggc tca cag gag ctg cct agg gag aag       1200
      Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys
      385             390             395             400

      tac ctg act tgg gca tcc cgg cag gag ccc agc caa ggc acc acc acc       1248
      Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr
```

```
                405                      410                      415
ttc gct gtg acc tcg ata ctg cgc gtg gca gcc gag gac tgg aag aag        1296
Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys
            420                  425                  430

ggt gac acc ttc tcc tgc atg gtg ggc cac gag gcc ctt ccg ctg gcc        1344
Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala
            435                  440                  445

ttc aca cag aag acc atc gac cgc                                        1368
Phe Thr Gln Lys Thr Ile Asp Arg
    450                  455
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<210>  6
<211>  456
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Mature heavy chain sequence

<400>  6
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1                5                  10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Ser Phe Ser Ser Tyr
            20                  25                  30

Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Gly Leu Met Pro Ile Phe Gly Thr Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Asp Arg Leu Thr Ile Thr Ala Asp Val Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Gln Leu Ser Gly Leu Thr Tyr Glu Asp Thr Ala Met Tyr Tyr Cys
            85                  90                  95

Ala Arg Val Ala Tyr Met Leu Glu Pro Thr Val Thr Ala Gly Gly Leu
            100                 105                 110

Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Pro
        115                 120                 125

Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Cys Ser Thr Gln Pro Asp
    130                 135                 140

Gly Asn Val Val Ile Ala Cys Leu Val Gln Gly Phe Phe Pro Gln Glu
145                 150                 155                 160

Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Gly Val Thr Ala Arg
            165                 170                 175

Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr Thr Thr Ser
            180                 185                 190

Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Leu Ala Gly Lys Ser Val
```

```
                    195                      200                      205
       Thr Cys His Val Lys His Tyr Thr Asn Pro Ser Gln Asp Val Thr Val
           210             215                 220

       Pro Cys Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro
       225             230                 235                     240

       Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser Leu His Arg
                   245                 250                     255

       Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Asn Leu Thr Cys
                   260                 .265                    270

       Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe Thr Trp Thr
                   275·                280                 285

       Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Glu Arg Asp Leu
           290             295                 300

       Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala Glu Pro
       305             310                 315                     320

       Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser
                   325                 330.                    335

       Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg
                   340                 345  .              350

       Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn
           355                 360                 365

       Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp
           370                 375                 380

       Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys
       385                 390                 395                     400

       Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr
                   405                 410                 415

       Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys
                   420                 425                 430

       Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala
                   435                 440                 445

       Phe Thr Gln Lys Thr Ile Asp Arg
           450         .       455
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<210> 7
<211> 69
<212> DNA
<213> Artificial sequence

<220>
<223> heavy chain tailpiece

<220>
<221> CDS

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<222>  (1)..(69)
<223>

<400>  7
ttg gcg ggt aaa ccc acc cat gtc aat gtg tct gtt gtc atg gcg gag        48
Leu Ala Gly Lys Pro Thr His Val Asn Val Ser Val Val Met Ala Glu
1               5                   10                  15

gtg gac ggc acc tgc tac tga                                            69
Val Asp Gly Thr Cys Tyr
            20


<210>  8
<211>  22
<212>  PRT
<213>  Artificial sequence

<220>
<223>  heavy chain tailpiece

<400>  8
Leu Ala Gly Lys Pro Thr His Val Asn Val Ser Val Val Met Ala Glu
1               5                   10                  15

Val Asp Gly Thr Cys Tyr
            20


<210>  9
<211>  702
<212>  DNA
<213>  Herpes simplex virus

<220>
<221>  CDS
<222>  (1)..(702)
<223>

<220>
<221>  misc_feature
<223>  HSV light chain sequence

<400>  9
atg gga tgg tcc tgg atc ttt ctc ttc ctt ctg tca gga gct gca ggt        48
Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly
1               5                   10                  15

gtc cac tgc gag atc gtg ctc acg cag tct cca ggc acc ctg tct ttg        96
Val His Cys Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu
                20                  25                  30

tcg cca ggg gaa cgt gcc acc ctc tcc tgc cgg gcc agt cag tcc gtt       144
Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val
            35                  40                  45

tcc agc gcg tac ctt gcc tgg tac cag cag aag cct ggc caa gct ccc       192
Ser Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
        50                  55                  60

agg ctc ctc atc tat ggt gcg tcc agc agg gct act ggc att cca gac       240
```

```
Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp
65              70              75              80

cgc ttc tca ggc agt ggg tct ggg aca gac ttc acg ctc acc att agc    288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
                85              90              95

agg ctg gaa cct gag gat ttt gca gtg tac tac tgt cag cag tat ggt    336
Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly
            100             105             110

cgc tca ccc acg ttc ggc cag ggg acc aag gtg gag atc aag cgc act    384
Arg Ser Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
            115             120             125

gtg gct gca ccg tcg gtc ttc ata ttc ccg cca tcc gat gag cag ctg    432
Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
    130             135             140

aag tct ggc act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccg    480
Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
145             150             155             160

aga gag gcg aag gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt    528
Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
                165             170             175

aac tcc caa gag tcc gtt aca gag cag gac agc aag gac agc acc tac    576
Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
            180             185             190

agc ctc agc aac acc ttg acg ctg agc aaa gcg gac tac gag aaa cac    624
Ser Leu Ser Asn Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
            195             200             205

aag gtc tac gcc tgc gaa gtc acc cat caa ggc ctg cgc tcg ccc gtc    672
Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Arg Ser Pro Val
    210             215             220

aca aag agc ttc aac cgg gga gag tgt tga                            702
Thr Lys Ser Phe Asn Arg Gly Glu Cys
225             230
```

```
<210>  10
<211>  233
<212>  PRT
<213>  Herpes simplex virus

<400>  10
Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly
1               5               10              15

Val His Cys Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu
            20              25              30

Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val
        35              40              45

Ser Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
    50              55              60
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```
Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp
65              70              75              80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
              85              90              95

Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly
        100             105             110

Arg Ser Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
        115             120             125

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
    130             135             140

Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
145             150             155             160

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
            165             170             175

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
            180             185             190

Ser Leu Ser Asn Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
        195             200             205

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Arg Ser Pro Val
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Thr Lys Ser Phe Asn Arg Gly Glu Cys
225             230
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<222>  (1)..(57)
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1               5               10              15

gtc cac tgc                                                        57
Val His Cys


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<212>  PRT
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Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly
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Val His Cys


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<212>  DNA
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Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
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gaa cgt gcc acc ctc tcc tgc cgg gcc agt cag tcc gtt tcc agc gcg       96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ala
                20                  25                  30

tac ctt gcc tgg tac cag cag aag cct ggc caa gct ccc agg ctc ctc      144
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
                35                  40                  45

atc tat ggt gcg tcc agc agg gct act ggc att cca gac cgc ttc tca      192
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
            50                  55                  60

ggc agt ggg tct ggg aca gac ttc acg ctc acc att agc agg ctg gaa      240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80

cct gag gat ttt gca gtg tac tac tgt cag cag tat ggt cgc tca ccc      288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Arg Ser Pro
                85                  90                  95

acg ttc ggc cag ggg acc aag gtg gag atc aag cgc act gtg gct gca      336
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
                100                 105                 110

ccg tcg gtc ttc ata ttc ccg cca tcc gat gag cag ctg aag tct ggc      384
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
            115                 120                 125

act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccg aga gag gcg      432
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
            130                 135                 140
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145                 150                 155                 160

gag tcc gtt aca gag cag gac agc aag gac agc acc tac agc ctc agc          528
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                    165                 170                 175

aac acc ttg acg ctg agc aaa gcg gac tac gag aaa cac aag gtc tac          576
Asn Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
                180                 185                 190

gcc tgc gaa gtc acc cat caa ggc ctg cgc tcg ccc gtc aca aag agc          624
Ala Cys Glu Val Thr His Gln Gly Leu Arg Ser Pro Val Thr Lys Ser
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ttc aac cgg gga gag tgt                                                   642
Phe Asn Arg Gly Glu Cys
210
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            20                  25                  30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
            35                  40                  45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
        50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Arg Ser Pro
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
                100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
            115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
        130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
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                  165                    170                    175
Asn Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                    185                    190
Ala Cys Glu Val Thr His Gln Gly Leu Arg Ser Pro Val Thr Lys Ser
            195                    200                    205
Phe Asn Arg Gly Glu Cys
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<213>  Artificial sequence

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accatatgcg gtgtgaaata ccgcacagat gcgtaaggag aaaataccgc atcaggcgcc  240

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tacgccagct ggcgaaaggg ggatgtgctg caaggcgatt aagttgggta acgccagggt  360

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cgcgattaaa aatcccaatt atatttggtc taatttagtt tggtattgag taaaacaaat  480

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<210> 19
<211> 122
<212> PRT
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<220>
<223> Heavy chain V region FabSHV 8

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Val Ser Cys Lys Ala Ser Gly Gly Ser Phe Ser Ser Tyr Ala Ile Asn
            20   25   30

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            35   40   45

Met Pro Ile Phe Gly Thr Thr Asn Tyr Ala Gln Lys Phe Gln Asp Arg
        50   55   60

Leu Thr Ile Thr Ala Asp Val Ser Thr Ser Thr Ala Tyr Met Gln Leu
65   70   75   80

Ser Gly Leu Thr Tyr Glu Asp Thr Ala Met Tyr Tyr Cys Ala Arg Val
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Ala Tyr Met Leu Glu Pro Thr Val Thr Ala Gly Gly Leu Asp Val Trp
            100   105   110

Gly Gln Gly Thr Thr Val Thr Val Ala Ser
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<210> 20
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<212> PRT
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<220>
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<400> 20

Asp Leu Leu Leu Gly Ser Glu Ala Asn Leu Thr Cys Thr Leu Thr Gly
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Leu Arg

<210> 21
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<220>
<223> peptide tryptic fragment L-T1

<400> 21
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1   5   10   15

Glu Arg

<210> 22
<211> 6
<212> PRT
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<220>
<223> peptide tryptic fragment L-T2

<400> 22
Ala Thr Leu Ser Cys Arg
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<210> 23
<211> 22
<212> PRT
<213> Artificial sequence

<220>
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<400> 23
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Pro Gly Gln Ala Pro Arg
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<210> 24
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> peptide tryptic fragment L-T4

<400> 24
Leu Leu Ile Tyr Gly Ala Ser Ser Arg
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<211>  7
<212>  PRT
<213>  Artificial sequence

<220>
<223>  peptide tryptic fragment L-T5

<400>  25
Ala Thr Gly Ile Pro Asp Arg
1               5


<210>  26
<211>  16
<212>  PRT
<213>  Artificial sequence

<220>
<223>  peptide tryptic fragment L-T6

<400>  26
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg
1               5                   10                  15


<210>  27
<211>  16
<212>  PRT
<213>  Artificial sequence

<220>
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<400>  27
Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Arg
1               5                   10                  15


<210>  28
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<212>  PRT
<213>  Artificial sequence

<220>
<223>  peptide tryptic fragment L-T8

<400>  28
Ser Pro Thr Phe Gly Gln Gly Thr Lys
1               5


<210>  29
<211>  18
<212>  PRT
<213>  Artificial sequence

<220>
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<400> 29
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1   5   10   15

Leu Lys

<210> 30
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<212> PRT
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<220>
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<400> 30
Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
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<210> 31
<211> 4
<212> PRT
<213> Artificial sequence

<220>
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<400> 31
Val Gln Trp Lys
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<210> 32
<211> 20
<212> PRT
<213> Artificial sequence

<220>
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<400> 32
Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
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Gln Asp Ser Lys
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<210> 33
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<212> PRT
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<220>
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<400> 33
Asp Ser Thr Tyr Ser Leu Ser Asn Thr Leu Thr Leu Ser Lys
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<220>
<223>  peptide tryptic fragment L-T17

<400>  34
Ala Asp Tyr Glu Lys
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<210>  35
<211>  12
<212>  PRT
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<220>
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<400>  35
Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Arg
1               5                   10


<210>  36
<211>  5
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<220>
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<400>  36
Ser Pro Val Thr Lys
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<210>  37
<211>  4
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<220>
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<400>  37
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<210>  38
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<220>
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Phe Thr Leu Thr Ile Ser Arg
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<400>  39
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg
1               5                   10                  15

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Arg
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1               5                   10


<210>  41
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Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1               5                   10                  15

Gln Leu Lys


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Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
1               5                   10                  15

Glu Ala Lys


<210>  43
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<212>  PRT
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<220>
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<400>  43
Glu Ala Lys Val Gln Trp Lys
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<210>  44
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<212>  PRT
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<400>  44
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
1               5                   10                  15

Ser Val Thr Glu Gln Asp Ser Lys
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<210>  45
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<400>  45
Ala Asp Tyr Glu Lys His Lys
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<210>  46
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<220>
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<400>  46
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Arg
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<212>  PRT
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Ser Pro Val Thr Lys Ser Phe Asn Arg
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<210>  48
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Ser Phe Asn Arg Gly Glu Cys
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Lys Pro Gly Ser Ser Val Lys
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<400> 51
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<210> 52
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<212> PRT
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<220>
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<400> 52
Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Leu Met Pro Ile
1   5   10   15

Phe Gly Thr Thr Asn Tyr Ala Gln Lys
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<210> 53
<211> 4
<212> PRT
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<220>
<223> peptide tryptic fragment H-T6

<400> 53
Phe Gln Asp Arg
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<210> 54
<211> 31
<212> PRT
<213> Artificial sequence

<220>
<223> peptide tryptic fragment H-T7

<400> 54
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1   5   10   15

Ser Gly Leu Thr Tyr Glu Asp Thr Ala Met Tyr Tyr Cys Ala Arg
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<210> 55
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<220>
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<400> 55
Val Ala Tyr Met Leu Glu Pro Thr Val Thr Ala Gly Gly Leu Asp Val
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Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Pro Thr Ser
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Pro Lys
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<210> 56
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<212> PRT
<213> Artificial sequence

<220>
<223> peptide tryptic fragment H-T9

<400> 56
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              20                  25                  30

Thr Trp Ser Glu Ser Gly Gln Gly Val Thr Ala Arg
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<210> 57
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<212> PRT
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<220>
<223> peptide tryptic fragment H-T10

<400> 57
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<220>
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<400> 58
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Ser Val Thr Cys His Val Lys
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<210> 59
<211> 38
<212> PRT
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<220>

<223> peptide tryptic fragment H-T12

<400> 59
His Tyr Thr Asn Pro Ser Gln Asp Val Thr Val Pro Cys Pro Val Pro
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Ser Cys Cys His Pro Arg
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<210> 60
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<212> PRT
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<220>
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